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Biogeosciences Discussions

Interactive comment on "Response of bacterioplankton community structure to an artificial gradient of pCO_2in the Arctic Ocean" *by* R. Zhang et al.

R. Zhang et al.

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Response to general comments of referee 1: We thank the referee for the generally positive comments and constructive contribution. We realized that the background information of the experimental setup and related biological parameters are lacking in previous version of our manuscript, which is the major concern raised by referee 1. In the revised manuscript, we provided necessary information to help readers understand our story without referring to accompanying papers frequently. However, it is also necessary to state that this a contribution to a special volume dealing with the Svalbard ocean acidification and that we have to refer to submitted/accepted pa-

pers (Final papers: http://www.biogeosciences.net/special_issue120.html Discussion papers: http://www.biogeosciences-discuss.net/special_issue94.html) since it cannot be the aim of publications to repeat data. Response to specific comments of referee 1: 1. Details on the experimental set-up are lacking, and while the authors refer to another paper they should anyway briefly explain the experimental set-up: motivations for the different treatments, the sizes of the mesocosms, where were they located; at which depth the samples for bacterial community were taken and when exactly the 19 samplings were performed. The author should also explain the motivation for the lack of replication of the mesocosm treatments and the issues related to this. Response: We agreed with the comments. A brief introduction of experimental setup, with all necessary information, are presented in the first two paragraphs of "Materials and methods" in the revised manuscript.

2. A significant part of the discussion is based on the 3 phases defined from chl. a concentrations in an accompanying paper. A figure or table reporting chl a data is essential for understanding this discussion. The figure could show the 3 phases and be adapted from Schulz, et al. 2012. Likewise, the figure could include bacterial abundance, which appears as another essential background parameter. Response: We added a figure panel showing three phases of Chl a, adapted from Schulz et al., 2012, in Fig. 1 in the revised manuscript. Since bacterial abundance did not show similar patterns, we did not include it and the readers can obtain this information from our description and a reference of same special issue. We have refered to accompanying papers in the revised version.

3. The choice of the samples for the Smax/Hmax analyses is very unclear and should be explained in more detail (specifically on p10652). Are these data from the same time point for the different treatments? Or at different time points? In that case which and during which phase? Or do they simply represent the time points at which diversity/richness was highest? Please, clarify in the text. Response: The calculation of Smax/Hmax is explained in detail in the new version of manuscript. Briefly, they

occurred at different time points of Phase 3 in different treatments. This difference suggests possible effects of pCO2 levels on the development of bacterial communityies.

4. Why were only the 30-day samples used for clone libraries and not the samples used for the Smax/Hmax study? Please, explain the choice of samples and the reasoning behind it. Response: In our study, clone library analysis was not used as a quantitative tool to investigate the bacterial community composition (BCC) due to limited sequencing size, as shown by the unsaturated asymptotic rarefaction curves in Fig. S2. However, we used the sequencing information from clone library analysis to infer the phylogenetic affiliation of T-RFs in T-RFLP analysis. In addition, we want to see whether OA will affect BCC after one month incubation, i.e. the maximum experimental timespan possible. Therefore, we used samples from Day 30 for clone library analysis which was used to provide phylogenetic assignment for T-RFLP analysis of Day 30 samples.

5. From the Trflp and clone library results the pCO2 concentrations had only minor effects on the dominant bacterial taxa over 30 days. The authors discuss that the lack of strong responses could be due to the coupling to phytoplankton only in the very last sentence. The issue of the phytoplankton bloom and its eventual effects should be discussed earlier. In particular, the authors could note the lack of a BIOENV correlation between bacterial community composition and phytoplankton biomass indicates that the response in bacterial community composition is not directly linked to phytoplankton biomass. Was phytoplankton biomass included in the BIOENV analysis? Please, clarify. What about the interactions of other trophic levels? Response: In general, our data suggest that Chl a (phytoplankton biomass) determined the diversity and taxonomic richness while complex biological and chemical factors affected the BCC (BIOENV analysis). The interactions of multi-trophic levels were observed in our BIOENV analysis (e.g. viruses (VBR), bacteria (BA), phytoplankton (DMS), etc.). We re-constructed the discussion part in the revised manuscript to make this clear.

6. The results of the sister stories from Sperling, et al and Piontek, et al in the same

issue of BG showed no effect of the different treatments on free living bacteria or a top down control of bacteria, respectively. These results seem to be highly relevant for the present story and should therefore be described in more detail in the present paper. Response: We agree with the reviewer and discuss the related content from Sperling, et al., Piontek, et al. and those from Roy et al., Brussaard et al. etc. in the revised manuscript.

7. Technical corrections: - In the introduction (l. 23) the reference for the microbial loop should be Azam et al. 1983. - In the material and methods the calculation for richness index and ANOSIM should be explained briefly (paragraph 2.3) - The different groups of mesocosms (high, medium, low pCO2) should be explained earlier in the material and methods (not in the results), so the reader can understand the different colors in the figures. Maybe the different groups could also be reminded in the figures. - P10656, l22-25. Unclear. Please, rephrase - P10657, l28 – P10658, l7. This section on cyanobacteria is highly speculative since no conclusions can be drawn upon the very few cyanobacterial sequences obtain. Please, delete this section. - Fig. 3. Define richness and diversity indices in the legend. - A and B needs to be added to Fig. 4 and to the Fig. 4 figure text. - Fig. 5. Is this the abundance relative to the sum of all peaks? Response: All comments raised by reviewer 1 were revised.

Interactive comment on Biogeosciences Discuss., 9, 10645, 2012.